

5 PAGE BLANK (uspto)

Db 1 TAGGCTTAACCTGGATCTACAGCCAAAGTCCCTCCCTGCTGAGGCGAGTACCCCTC 60

Qy 7694 cattggcacagctccagaccagctcaagatgccctcttgcctcagccctcag 7753
|||||
Db 61 -CATTGSCACAGTCCACACCAAGTCAAGATGCCCATCTCTTGCCTCAGCCCTCAG 120
|||||

Qy 7754 ttctctcattccaccagcgctgcttcttggagtttttctctccagtgag 7805
|||||
Db 121 TTCTCTCATTCCACAGGCGCTGCTTGTGAGTTTCTCTCCAGTGAG 172
|||||

RESULT 9
AF123652 231 bp mRNA PRI 07-APR-1999

LOCUS Homo sapiens clone E1678 FE21 (FE21) mRNA, alternatively spliced,
complete cds.

ACCESSION AF123652
VERSION AF123652.1 GI:4572461

KEYWORDS human.

SOURCE Homo sapiens

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 231)

AUTHORS Ishii, H., Baffa, R., Numata, S.I., Murakumo, Y., Rattan, S., Inoue, H.,
Mori, M., Fidanza, V., Alder, H. and Croce, C.M.

TITLE The FE21 gene at chromosome 8p22 encodes a leucine-zipper protein,
and its expression is altered in multiple human tumors

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (7), 3928-3933 (1999)

MEDLINE 99199287

REFERENCE 2 (bases 1 to 231)

AUTHORS Ishii, H., Baffa, R., Numata, S.I., Murakumo, Y., Rattan, S., Inoue, H.,
Mori, M., Fidanza, V., Alder, H. and Croce, C.M.

TITLE Direct Submission

JOURNAL Submitted (27-JAN-1999) Immunology/Microbiology, Kimmel Cancer
Institute, 233S 10th street, Philadelphia, PA 19107, USA

FEATURES
source
1..231
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="8"
/map="8p22"
/clone="E1678"
1..231
/gene="FE21"
1..231
/gene="FE21"
/note="alternatively spliced."
/codon_start=1
/product="FE21"
/protein_id="AAD23833.1"
/db_xref="GI:4572462"
/translation="MGVSLLISGHSHKCRASOYKLRKSSHLKLNRYSDGLLR
FGSDSHGKAMTRCPRSSMSGCGRRRRR"
50 a 70 c 70 g 41 t

BASE COUNT 50 a 70 c 70 g 41 t

ORIGIN
Query Match 1.8%; Score 162; DB 40; Length 231;
Best Local Similarity 100.0%; Pred. No. 6e-79;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 52 atgggcagcgtcagtagctcctccgcccacagcttccacagcaagcactgcccggct 111
|||||

Db 1 ATGGCAGCGCTCAGTAGCTCTATCTCCGCCACAGCTTCCACAGCAGCAGCTGCCGGCT 60
|||||

Qy 112 tcgcagtaaacgtcgcagctcctccacccctcaagaagctcaaccggtattccgacgg 171
|||||

Db 61 TCGCAGTACAAAGCTGGCAGAGTCCCTCCACCTCAAGAGCTCAACCGGTATTCGACGG 120
|||||

Qy 172 ctgctgaggttggcttctccaggagactccggtcagcggaag 213
|||||

Db 121 CTGCTGAGGTTTGCTTCTCCAGGAGCTCCGGTCCAGGCAAG 162
|||||

RESULT 10

G43056

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

COMMENT

Synonyms: stSG10118

Contact: Thomas Hudson

Whitehead Institute/MIT Center for Genome Research

Whitehead Institute for Biomedical Research

9 Cambridge Center, Cambridge MA 02142 USA

Tel: 617 252 1900

Fax: 617 252 1902

Email: thudson@genome.wi.mit.edu

Primer A: TAGGCTTAACCTGGATCTAC

Primer B: CTCACCTGGGAGGAAAAC

STS size: 172

PCR Profile:

Presoak: 94 degrees C for 4.00 minutes

Denaturation: 58 degrees C for 50.0 seconds

Annealing: 58 degrees C for 1.50 minutes

Polymerization: 72 degrees C for 1.00 minutes

PCR Cycles: 30

Thermal Cycler: custom built by IAS, Costar, Cambridge MA

Protocol:

Template: 10 ng

Primer: each 5 pM

dNTPs: 4 mM

Tag Polymerase: 0.5 U

Total Vol: 20 uL

Buffer:

Mg2+: 1.5 mM

KCl: 50 mM

Tris-HCl: 10 mM

Gelatin: .001 %

Location/Qualifiers

1..172

/organism="Homo sapiens"

/db_xref="taxon:9606"

/map="42.70 cR from top of Chr8 linkage group"

/clone.lib="Human THudson SANGER"

/note="human STS created from EST in the Sanger database"

1..172

primer_bind

primer_bind

complement(155..172)

BASE COUNT 36 a 58 c 34 g 43 t

ORIGIN

Query Match 1.3%; Score 121; DB 13; Length 172;

Best Local Similarity 99.4%; Pred. No. 5.3e-56;

Matches 171; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

IN nucleic - nucleic search, using sw model

Run on: April 19, 2000, 22:46:09 ; Search time 4891.93 Seconds

(Without alignments)
-5616.025 Million cell updates/sec

Title: PCT-US00-04950-1
Effect score: 9048
Sequence: 1 gcccttccagaacctgcctcc.....tgccattctcagccctct 9048

Coring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

searched: 821193 seqs, -1518192014 residues

ord size : 0

total number of hits satisfying chosen parameters: 1642386

inlunum DB seq length: 0
axlunum DB seq length: 1000000

ost-processing: Listing first 45 summaries

database :

GenFtbl:.*
1: gb_ba1.*
2: gb_ba2.*
3: gb_om.*
4: gb_ov.*
5: gb_pat.*
6: gb_ph.*
7: gb_pl1.*
8: gb_pl2.*
9: gb_pl3.*
10: gb_pl4.*
11: gb_pl5.*
12: gb_pl6.*
13: gb_pl7.*
14: gb_pl8.*
15: gb_pl9.*
16: gb_pl10.*
17: gb_pl11.*
18: gb_pl12.*
19: gb_pl13.*
20: gb_pl14.*
21: gb_pl15.*
22: gb_pl16.*
23: gb_pl17.*
24: gb_pl18.*
25: gb_pl19.*
26: gb_pl20.*
27: gb_pl21.*
28: gb_pl22.*
29: gb_pl23.*
30: gb_pl24.*
31: gb_pl25.*
32: gb_pl26.*
33: gb_pl27.*
34: gb_pl28.*
35: gb_pl29.*
36: gb_pl30.*
37: gb_pl31.*
38: gb_pl32.*
39: gb_pl33.*
40: gb_pl34.*
41: gb_pl35.*
42: gb_pl36.*
43: gb_pl37.*

44: gb_htg6.*
45: gb_htg7.*
46: em_htg1.*
47: em_htg2.*
48: em_htg3.*
49: em_hum5.*
50: gb_pl3.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	9048	100.0	9108	40	AF123653 Homo sapi
2	4097	45.3	5492	40	AF123659 Homo sapi
3	757	8.4	1515	40	AF123656 Homo sapi
4	757	8.4	1614	40	AF123655 Homo sapi
5	757	8.4	1692	40	AF123657 Homo sapi
6	757	8.4	1722	40	AF123658 Homo sapi
7	346	3.8	633	40	AF123654 Homo sapi
8	172	1.9	172	13	G60003 Homo sapi
9	162	1.8	231	13	AF123652 Homo sapi
10	121	1.3	172	13	G43056 Homo sapi
11	98	1.1	250	13	G15289 Homo sapi
12	57	0.6	53967	42	AC012422 Homo sapi
13	57	0.6	165836	42	AC011963 Homo sapi
14	57	0.6	185893	11	AC005191 Homo sapi
15	55	0.6	197541	41	AC011371 Homo sapi
16	54	0.6	177596	33	HS88517 Homo sapi
17	53	0.6	37918	41	AC011553 Homo sapi
18	53	0.6	98261	10	HS1054C24 Homo sapi
19	52	0.6	123585	11	AC004707 Homo sapi
20	51	0.6	100267	40	HS88517 Homo sapi
21	51	0.6	129811	32	HS167P19 Homo sapi
22	51	0.6	130082	32	HS167P19 Homo sapi
23	51	0.6	144387	33	HS88517 Homo sapi
24	51	0.6	183285	42	AC009833 Homo sapi
25	50	0.6	132418	33	AC006357 Homo sapi
26	50	0.6	164905	42	AC007097 Homo sapi
27	50	0.6	187278	44	AC010192 Homo sapi
28	49	0.5	154347	43	AC013612 Homo sapi
29	49	0.5	168385	43	AC011857 Homo sapi
30	49	0.5	186711	43	AC011857 Homo sapi
31	49	0.5	205439	41	AC011400 Homo sapi
32	49	0.5	264977	42	AC009061 Homo sapi
33	48	0.5	483	9	HS88517 Homo sapi
34	48	0.5	56078	32	HS167P19 Homo sapi
35	48	0.5	86408	33	AC007952 Homo sapi
36	48	0.5	98240	40	AC006021 Homo sapi
37	48	0.5	119694	32	HS167P19 Homo sapi
38	48	0.5	172048	10	HS179N16 Homo sapi
39	48	0.5	177540	40	AC006538 Homo sapi
40	48	0.5	179865	41	AC007375 Homo sapi
41	48	0.5	184939	44	AC013682 Homo sapi
42	48	0.5	192612	41	AC008569 Homo sapi
43	48	0.5	256694	41	AC009280 Homo sapi
44	48	0.5	298966	32	HS167P19 Homo sapi
45	47	0.5	101215	40	AC006966 Homo sapi

ALIGNMENTS

RESULT 1
AF123653
LOCUS AF123653 9108 bp DNA
DEFINITION Homo sapiens FEZ1 (FEZ1) gene, complete cds.
ACCESSION AF123653
VERSION AF123653.1 GI:4572463

07-APR-1999

Db	1	TAGGCTTAAACCTGGGAATCTTACAAGCCAAAGTCTCCTTCCTGCTGAGGGCAGTACCCTC	60
Qy	7694	catgggcacagctccagaccacaaagtcaaaagatgccccattctctgcctcagccctcag	7753
Db	61	CATTGGGCACACTCAGACCCCAAGTCAAGATGCCCCATTCCTTGGCTCAGCCCTCAG	120
Qy	7754	tctcttcatttccacacagccgctgcctgtttgagttttctctccagtgag	7805
Db	121	TTCCCTTCATTCCACAGCCGCTGCTTGTGTTGAGTGTTCCTCCAGTGAG	172
RESULT	9		
AF123652			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
MEDLINE			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
FEATURES			
source			
gene			
CDS			
BASE COUNT	50	a 70	c 70
ORIGIN			
Query Match			
Best Local Similarity	1.88;	Score 162;	DB 40; Length 231;
Matches 162;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
Qy	52	atgggcagcgcagtagcctcatctccggccacagcttccacagcactgcgcggcct	111
Db	1	ATGGCAGCGTCAGTAGGCTCATCTCCGGCCACAGCTTCCACAGCAGCAGCTCGCGGCT	60
Qy	112	tcgcagtcacagctgcgcgaagtccctccacatcccaagagctcaaccgggtatccgacggg	171
Db	61	TCGCAGTACAGCTCGCGCAAGTCTCCACCTCAAGAAGCTCAACCGGTATTCGACGGG	120
Qy	172	ctgctgaggtttggtttctccaggaactccggctcagggcaag	213
Db	121	CTGCTGAGGTTGGCTTCTCCAGGACTCCGGTCAAGCAAG	162

http://ftp.genome.washington.edu/RV/RepeatMasker.html.

* NOTE: This record contains 70 individual

* sequencing reads that have not been assembled into

* contigs. Runs of N are used to separate the reads

* and the order in which they appear is completely

* arbitrary. Low-pass sequence sampling is useful for

* identifying clones that may be generic and allows

* overlap relationships among clones to be deduced.

* However, it should not be assumed that this clone

* will be sequenced to completion. In the event that

* the record is updated, the accession number will

* be preserved.

* 1

722:	contig of 722 bp in length
	gap of unknown length
723	1504: contig of 782 bp in length
	gap of unknown length
1505	2265: contig of 761 bp in length
	gap of unknown length
2266	3025: contig of 760 bp in length
	gap of unknown length
3026	3791: contig of 766 bp in length
	gap of unknown length
3792	4608: contig of 817 bp in length
	gap of unknown length